

REMARKS

Claims 1-3, 48, and 57 have been amended and claim 59 has been added. Claims 9, 12-45, 49-54, and 56 have been canceled without prejudice or disclaimer. Claims 1-8, 10, 11, 48, 55, and 57-59 are pending in the instant application. Support for the amendments to the claims can be found in the specification at, for example, page 32 (Table I), page 35, lines 21-27, and in Figures 1-7 and 9. No new matter has been added as a result of the above-described amendments. The rejections set forth in the Office Action have been overcome by amendment or are traversed by argument below.

1. Rejections of claims 1-8, 10, 11, 48, 55, 57, and 58 under 35 U.S.C. § 112, first paragraph

The Office Action asserts a rejection of claims 1-8, 10, 11, 48, 55, 57, and 58 under 35 U.S.C. § 112, first paragraph, as containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention. The Action states that because one of ordinary skill in the art cannot envision the detailed structure of a genus of polynucleotide variants comprising allelic or splice variants of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5; sequences that are at least 70% identical to SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5; or sequences that hybridize under at least moderately stringent conditions to the complement of a nucleotide sequence encoding a polypeptide having an activity of the polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6, the specification does not meet the written description requirement for claiming such genera. Specifically, the Action states that because these genera are highly variant, the species disclosed in SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 5 are not representative of these genera.

Applicants have amended claim 1 to recite an isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5; a nucleotide sequence encoding a polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6; or a nucleotide sequence that is complementary to the nucleotide sequence of either of these nucleic acid molecules. Applicants contend that because claim 1, as amended, no longer recites an isolated nucleic acid molecule comprising a nucleotide sequence that hybridizes under at least moderately stringent conditions to the complement of a nucleotide sequence encoding a polypeptide having an activity of

the polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6, amended claim 1 satisfies the requirements of 35 U.S.C. § 112, first paragraph.

Applicants have amended claim 2 to recite an isolated nucleic acid molecule comprising a region of the nucleotide sequence of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5 encoding a polypeptide fragment of at least 25 amino acid residues, wherein the polypeptide fragment has an activity of a polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6, or is antigenic; a region of the nucleotide sequence of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5 comprising a fragment of at least 16 nucleotides; or a nucleotide sequence that is complementary to the nucleotide sequence of either of these nucleic acid molecules. Applicants contend that because claim 2, as amended, no longer recites allelic or splice variants of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5; sequences that are at least 70% identical to SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5; or sequences that hybridize under at least moderately stringent conditions to the complement of a nucleotide sequence encoding a polypeptide having an activity of the polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6, amended claim 2 satisfies the requirements of 35 U.S.C. § 112, first paragraph.

Applicants have similarly amended claim 3 so that it no longer recites an isolated nucleic acid molecule comprising a nucleotide sequence that hybridizes under at least moderately stringent conditions to the complement of a nucleotide sequence encoding a polypeptide having an activity of the polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6. Applicants, therefore, respectfully contend that amended claim 3 also satisfies the requirements of 35 U.S.C. § 112, first paragraph.

In addition, Applicants wish to direct the Examiner's attention to new claim 59, which has been added to more particularly point out and distinctly claim the subject matter that Applicants regard as the invention. The amino acid sequence recited in claim 59 is based on an amino acid sequence comparison of several murine and human B7-like polypeptides that indicates the structural features shared by these sequences (Appendix A). Applicants contend that the instant specification teaches one of ordinary skill in the art to perform a sequence comparison of the murine and human B7-like polypeptides disclosed in the instant specification in order to determine the positions within the human B7-like polypeptide sequence where substitutions, either conservative or nonconservative, would be tolerated, and that such a comparison was well within the skill of one having ordinary skill

in the art. Support for claim 59 can be found in the specification at, for example, page 32 (Table I), page 35, lines 21-27, and in Figures 1-7 and 9.

The Office Action also asserts a rejection of claims 1-8, 10, 11, 48, 55, 57, and 58 under 35 U.S.C. § 112, first paragraph, because the specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with the claims.

The Action first asserts that because the specification does not provide sufficient guidance (e.g., a functional assay) or evidence regarding B7-like activity, one of ordinary skill in the art could not reasonably determine whether any of the nucleic acid molecules encompassed by claims 1-3 encodes a polypeptide having B7-like activity, and therefore, would require undue experimentation to use the claimed nucleic acid molecules. The Action also asserts that because the specification does not provide sufficient guidance or evidence regarding the residues of B7-like polypeptide that are essential for B7-like activity, and because even a single amino acid substitution can have an unpredictable effect on polypeptide activity, one of ordinary skill in the art would require undue experimentation to identify polypeptides having B7-like activity, and therefore, would require undue experimentation to make the nucleic acid molecules encoding such polypeptides.

Applicants respectfully disagree with the Action's assertion that one of ordinary skill in the art could not reasonably determine whether any of the nucleic acid molecules encompassed by claims 1-3 encodes a polypeptide having B7-like activity. Applicants wish to direct the Examiner's attention to page 93, lines 7-9 of the specification, where Applicants teach that transgenic mice expressing a B7-like polypeptide exhibit seminal vesicle hyperplasia. Applicants, therefore, respectfully contend that in view of the specification's teachings, one of ordinary skill in the art could readily determine whether a specific nucleic acid molecule encodes a polypeptide having B7-like activity by expressing the molecule in a mouse and determining whether the mouse exhibits seminal vesicle hyperplasia. Applicants also disagree with the Action's assertion that the specification does not provide sufficient teaching regarding the residues of B7-like polypeptide that are essential for B7-like activity. As discussed above, Applicants contend that the specification teaches one of ordinary skill in the art to perform a sequence comparison of B7-like polypeptide orthologs in order to determine the positions within the human B7-like polypeptide sequence where amino acid substitutions are tolerated, and that such a comparison was well within the skill of one

having ordinary skill in the art. Applicants, therefore, respectfully contend that claims 1-3 fulfill the requirements of 35 U.S.C. § 112, first paragraph.

The Action next asserts that because gene therapy was unpredictable at the time the instant application was filed, and because the specification does not provide sufficient guidance or evidence correlating the modulation of B7-like polypeptide levels in an animal with a therapeutic effect in that animal, one of ordinary skill in the art would require undue experimentation to use the method of claim 55. The Action also asserts that because the term "modulating" encompasses increasing or decreasing the level B7-like polypeptides in an animal, and the specification does not provide sufficient guidance or evidence as to how the claimed nucleic acid molecules can be used to decrease B7-like polypeptide levels in an animal, one of ordinary skill in the art would require undue experimentation to use the method of claim 55.

Applicants respectfully disagree with the Action's assertion, and contend that one with skill in the art could readily practice the claimed method using, for example, B7-like antisense inhibitors or dominant negative mutants identified by the genetic suppressor element (GSE) screening approach disclosed in U.S. Patent Nos. 5,217,889 and 5,811,234 (to Roninson *et al.*). Applicants contend that nucleic acid molecules encoding dominant negative mutants could be used to decrease B7-like polypeptide levels in an animal. Applicants, therefore, respectfully request that this rejection be withdrawn.

The Action next asserts that while the specification is enabling for nucleotide sequences that hybridize under moderately or highly stringent conditions to the "full complement" of a nucleotide sequence encoding a polypeptide having B7-like activity, the specification is not enabling for nucleotide sequences that hybridize under moderately or highly stringent conditions to the "complement" of a nucleotide sequence encoding a polypeptide having B7-like activity. Specifically, the Action asserts that by using the term "complement," rather than the term "full complement," the nucleic acid molecules of claims 1(c), 2(e), and 3(g) read on any nucleic acid molecule comprising one or more nucleotides, including nucleic acid molecules that do not encode polypeptides possessing B7-like activity.

Applicants respectfully disagree with the Action's assertion that the complementary sequence of a nucleic acid molecule (*i.e.*, a nucleotide sequence complement) encompasses any sequence comprising one or more nucleotides of that nucleic acid molecule. Applicants contend that such a

meaning is contrary to the established meaning of the term “nucleotide sequence complement” in the art. For example, Alberts *et al.* describes a complementary sequence as “a mold of the original,” such that the sequence of nucleotides in a nucleic acid molecule is *preserved* in its complementary strand. Alberts *et al.*, *Molecular Biology of the Cell*, pp. 5-7 (Garland Publishing, Inc., 1994). Applicants, therefore, contend that the nucleotide sequence complement of the nucleotide sequence 5'-A-G-C-T-A-G-C-T-3' is well understood in the art to be 5'-T-C-G-A-T-C-G-A-3', and not one or more nucleotides of that nucleic acid molecule. Nevertheless, Applicants have amended claims 1-3, as described above, so that these claims no longer recite an isolated nucleic acid molecule comprising a nucleotide sequence that hybridizes under at least moderately stringent conditions to the complement of a nucleotide sequence encoding a polypeptide having an activity of the polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6. Applicants, therefore, respectfully contend that claims 1-3, as amended, fulfill the requirements of 35 U.S.C. § 112, first paragraph.

Applicants respectfully contend that rejections based on 35 U.S.C. § 112, first paragraph, have been overcome by amendment or traversed by argument, and request that the Examiner withdraw all rejections made on this basis.

2. Rejections of claims 1-3, 8, 10, and 55 under 35 U.S.C. § 112, second paragraph

The Office Action asserts a rejection of claims 1-3, 8, 10, and 55 under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter that Applicant regards as the invention.

The Action first asserts that claims 8, 10, and 55 are indefinite for reciting the term “B7-like polypeptide.” Applicants are unclear as to the basis of this rejection, since the Action *both* states that the specification does not define the term (page 16, lines 5-7) *and* that the specification defines the term using only amino acid sequences (*i.e.*, as indicated by sequence identifiers) without identifying a function or biological activity for these amino acid sequences (page 16, lines 7-9). However, in order to provide a reply to the instant Office Action that is fully responsive, Applicants address each of the Action’s assertions.

With regard to the Action’s assertion that the specification does not define the term “B7-like polypeptide,” Applicants wish to direct the Examiner’s attention to page 16, lines 23-28 of the specification, where the term is clearly defined as referring to “one or more recombinant human

polypeptides comprising the amino acid sequence of SEQ ID NOs: 2, 4, 6 or 8, related polypeptides thereto, or recombinant murine polypeptides comprising the amino acid sequence of SEQ ID NOs: 10, 11 or 12, and related polypeptides thereto.” The specification also defines “related polypeptides” at page 16, lines 29-32 as including “B7-like polypeptide allelic variants, B7-like polypeptide orthologs, B7-like polypeptide splice variants, B7-like polypeptide variants and B7-like polypeptide derivatives.” The specification further defines “B7-like polypeptide allelic variants,” “B7-like polypeptide orthologs,” “B7-like polypeptide splice variants,” “B7-like polypeptide variants,” and “B7-like polypeptide derivatives,” at page 17, lines 4-8; page 18, lines 20-25; page 18, lines 26-31; page 18, line 32 to page 19, line 7; and page 17, lines 9-15, respectively. As the specification clearly defines the term “B7-like polypeptide,” Applicants contend that claims 8, 10, and 55 are *not* indefinite for reciting this term and respectfully request withdrawal of this ground of rejection.

Applicants next address the Action’s assertion that the specification defines the term “B7-like polypeptide” using only amino acid sequences without identifying a function or biological activity for these amino acid sequences. Applicants note that in light of the specification’s teachings (as discussed above), the term “B7-like polypeptide” describes a class of molecules comprising polypeptides having a particular amino acid sequence (e.g., the amino acid sequence of SEQ ID NO: 2) and related polypeptides having similar amino acid sequences. Applicants contend that because the term “B7-like polypeptide” describes a class of molecules using a characteristic property of that class (*i.e.*, amino acid sequence), the recitation of this term in the claims does not render those claims indefinite. Applicants therefore, respectfully request withdrawal of this ground of rejection.

The Action next asserts that there is insufficient antecedent basis in claims 1-3 for the phrase “the polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6. Applicants respectfully contend that because claims 1-3 have been amended as suggested in the Action to recite “a polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6,” this ground of rejection should be withdrawn.

The Action next asserts that there is insufficient antecedent basis in claims 1-3 for the phrase “the encoded polypeptide.” Applicants respectfully disagree with the Action’s assertion, and contend that the antecedent basis for the phrase “the encoded polypeptide” in, for example, line 4 of claim 3, is the phrase “a polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6 with at least one conservative amino acid substitution,” in lines 2-3. In other words, “the encoded

polypeptide" of claim 3(a) is the "polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6 with at least one conservative amino acid substitution" that is encoded by the nucleotide sequence of that subpart.

The Action next asserts that claims 48 and 57 are indefinite for reciting the phrase "a nucleic acid molecule of any of Claims 1, 2, or 3," because the phrase does not particularly point out which molecule "a nucleic acid molecule" refers to in the claim. Applicants respectfully contend that because claims 48 and 57 have been amended as suggested in the Action to recite "the nucleic acid molecule of any of Claims 1, 2, or 3," this ground of rejection should be withdrawn.

Applicants respectfully contend that rejections based on 35 U.S.C. § 112, second paragraph, have been overcome by amendment or traversed by argument, and request that the Examiner withdraw all rejections made on this basis.

3 . Rejections of claims 1-3 under 35 U.S.C. § 102

The Office Action asserts a rejection of claims 1-3 under 35 U.S.C. § 102(a), as being anticipated by Marra *et al.* (The Washington University-NCI Mouse EST project, seq_name: gb_est82:BF040046, July 2, 1999; GenBank Accession No. AI790785), contending that Marra *et al.* disclose an EST sequence that shares 85% similarity with the nucleotide sequences set forth in SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 5. The Action states that the sequence disclosed by Marra *et al.* reads on a "sequence that is complementary to any of the claimed sequences," since "[a] sequence that is complementary would encompass a nucleotide with one base pair or more in common with any claimed sequence." The Action also states that because of the breath of the phrase "an activity of the polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6," which encompasses any activity – including antigenicity, Marra *et al.* anticipates claims 1-3, since the sequence disclosed by Marra *et al.* is antigenic when administered to an animal.

Marra *et al.* disclose a nucleotide sequence of 530 bp. SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 5 set forth nucleotide sequences of 1146 bp, 1158 bp, and 1158 bp, respectively. Exhibits A-C indicate that there is an overlap of no more than 274 bp or 286 bp between the nucleotide sequence disclosed by Marra *et al.* and the nucleotide sequences set forth in SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 5. Exhibits A-C also indicate that in the overlapping regions, the sequences share an identity of between 69.6% to 72.6%, and *not* 85% (Applicants understand the

Office Action to mean 85% *identity*, rather than *similarity*, since the term “similarity” refers to the degree of sequence relatedness between two polypeptide sequences, and is defined as such in the instant specification at page 21, lines 6-20).

As discussed above in section 1 above, Applicants respectfully disagree with the Action’s assertion that the complementary sequence of a nucleic acid molecule (*i.e.*, a nucleotide sequence complement) encompasses any sequence comprising one or more nucleotides of that nucleic acid molecule. Applicants contend that such a meaning is contrary to the established meaning of the term “nucleotide sequence complement” in the art. Applicants, therefore, contend that the sequence of Marra *et al.*, which is *less than half* the length of the sequences of SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 5, and which shares an identity of between 69.6% and 72.6% with these sequences, *cannot* anticipate a nucleotide sequence that is complementary to the nucleotide sequence of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5. Moreover, Applicants contend that since none of the pending claims reads upon *any* polypeptide having “an activity of the polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6,” it is *not* sufficient, for Marra *et al.* to anticipate claims 1-3, that the sequence disclosed by Marra *et al.* merely be antigenic when administered to an animal. Rather, for Marra *et al.* to anticipate claims 1-3, the sequence disclosed by Marra *et al.* must meet each and every limitation of the claimed invention. Because Marra *et al.* does not disclose a sequence that meets each and every limitation of the claimed invention, Marra *et al.* *cannot* anticipate claims 1-3. Applicants, therefore, respectfully request that this ground of rejection be withdrawn.

The Office Action also asserts a rejection of claims 1-3 under 35 U.S.C. § 102(b), as being anticipated by Taudien *et al.* (GenBank Accession No. AF121782, published February 2, 1999), contending that “Taudien *et al.* disclose a nucleotide sequence that is complementary to the nucleotide sequences from SEQ ID NO[s]: 1-6.” The Action suggests that this rejection can be overcome by amending claims 1(d), 2(f), and 3(h) to replace the phrase “a nucleotide sequence complementary to the nucleotide sequence” with the phrase “a nucleotide sequence that is the full complement of the nucleotide sequence.”

Taudian *et al.* disclose a *genomic* sequence of 142,742 nucleotides for human chromosome 21q22.3 PAC 206A10. SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 5 set forth *cDNA* sequences for human B7-like polypeptide. Exhibits D-F indicate that the open reading frames of the

cDNA sequences of SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 5 (*i.e.*, the 1149-1161 nucleotide sequences encoding the amino acid sequences of SEQ ID NO: 2, SEQ ID NO: 4, and SEQ ID NO: 6) share an identity of between only 62.2 and 62.5% with the genomic sequence disclosed of Taudian *et al.*

As discussed above, Applicants respectfully disagree with the Action's assertion that the complementary sequence of a nucleic acid molecule (*i.e.*, a nucleotide sequence complement) encompasses any sequence comprising one or more nucleotides of that nucleic acid molecule. Because the genomic sequence of Taudian *et al.* shares an identity of between only 62.2 and 62.5% with the coding portion of the cDNA sequences of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5, Taudian *et al.* cannot anticipate claims directed to a nucleotide sequence that is complementary to the nucleotide sequence of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5. Applicants, therefore, respectfully request that this ground of rejection be withdrawn.

Applicants respectfully contend that rejections based on 35 U.S.C. § 102 have been traversed by argument, and request that the Examiner withdraw all rejections made on this basis.

CONCLUSIONS

Applicants respectfully contend that all conditions of patentability are met in the pending claims as amended. Allowance of the claims is thereby respectfully solicited.

If Examiner Whiteman believes it to be helpful, he is invited to contact the undersigned representative by telephone at (312) 913-0001.

Dated: April 2, 2003

Respectfully submitted,
McDonnell Boehnen Hulbert & Berghoff

By:

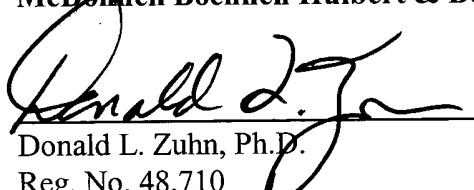

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EXHIBIT A

	10	20	30	40	50	60	
	*	*	*	*	*	*	*
SEQ01_ORF	ATGGGGCTTG	TGATTTCT	CCACGGTCT	GGGTCTGGTA	ATGAAGTCAT	AGAAGGCC	
	TACCCCGAAC	ACTAAAAGGA	GGTCCAAGA	CCCAGACCAT	TACTCAGTA	TCTTCCGGGG	
	260	270	280	290	300	310	
Marra EST	cTGGtcaTcc	TGgcTcagCT	gacaGcTTc	GGaTCcaGTt	ATcAgaTCAT	AGAAGGtCCT>	
SEQ01_ORF	ATGGGGCTTG	TGATTTCT	CCACGGTCT	GGGTCTGGTA	ATGAAGTCAT	AGAAGGCC	
	70	80	90	100	110	120	
	*	*	*	*	*	*	*
SEQ01_ORF	CAGAATGCAA	CAGTCCTGAA	GGGCTCCCAG	GCTCGCTTCA	ACTGCACCGT	CTCCCAGGGC	
	GTCCTACGTT	GTCAGGACTT	CCCGAGGGTC	CGAGCGAAGT	TGACGTGGCA	GAGGGTCCCG	
	320	330	340	350	360	370	
Marra EST	CAGAATGtAA	CAGTCCTAA	GGaCTCAGAG	GCTCaCTTCA	ACTGCACCGT	gaCtCAcGGC>	
SEQ01_ORF	CAGAATGCAA	CAGTCCTGAA	GGGCTCCCAG	GCTCGCTTCA	ACTGCACCGT	CTCCCAGGGC	
	130	140	150	160	170	180	
	*	*	*	*	*	*	*
SEQ01_ORF	TGGAAGCTCA	TCATGTGGC	TCTCAGTGAC	ATGGTGGTGC	TAAGCGTCAG	GCCCATGGAG	
	ACCTTCGAGT	AGTACACCCG	AGAGTCACTG	TACCACCACG	ATTCGCAGTC	CGGGTACCTC	
	380	390	400	410	420	430	
Marra EST	TGGAAGCTtc	TCATGTGGaC	TCTtAaccAa	ATGGTGGTGC	TgAGtcTCcc	aCCAAaGG-a>	
SEQ01_ORF	TGGAAGCTCA	TCATGTGGC	TCTCAGTGAC	ATGGTGGTGC	TAAGCGTCAG	GCCCATGGAG	
	190	200	210	220	230	240	
	*	*	*	*	*	*	*
SEQ01_ORF	CCCATCATCA	CCAATGACCG	CTTCACCTCT	CAGAGGTACG	ACCAGGGCGG	GAACTTCACC	
	GGGTAGTAGT	GGTTACTGGC	GAAGTGGAGA	GTCTCCATGC	TGGTCCCGCC	CTTGAAGTGG	
	440	450	460	470	480	490	
Marra EST	CCCATCATCA	CCAACAACCG	tTTCACCTaT	gccAGtTA-c	AaCAGcatGa	cAgCTTCAtC>	
SEQ01_ORF	CCCATCATCA	CCAATGACCG	CTTCACCTCT	CAGAGGTACG	ACCAGGGCGG	GAACTTCACC	
	250	260	270	280	290	300	
	*	*	*	*	*	*	*
SEQ01_ORF	TCGGAGATGA	TCATCCACAA	TGTGGAGCCC	AGTGATTGG	GGAACATCAG	ATGCAGCCTC	
	AGCCTCTACT	AGTAGGTGTT	ACACCTCGGG	TCACTAAGCC	CCTTGTAGTC	TACGTGGAG	
	500	510	520				
Marra EST	TCGGAGtTGA	TCATCCATgA	TGTGcAGCCC	AGTG>			
SEQ01_ORF	TCGGAGATGA	TCATCCACAA	TGTGGAGCCC	AGTG			

	310	320	330	340	350	360	
SEQ01_ORF	*	*	*	*	*	*	*
	CAGAACAGTC	GCCTGCATGG	ATCTGCTTAC	CTTACCGTCC	AAGTTATGGG	AGAGCTGTT	
	GTCTTGTCA	CGGACGTACC	TAGACGAATG	GAATGGCAGG	TTCAATACCC	TCTCGACAAG	
	370	380	390	400	410	420	
SEQ01_ORF	*	*	*	*	*	*	*
	ATTCCCAGTG	TTAATCTTGT	AGTCGCTGAG	AATGAACCTT	GTGAAGTTAC	TTGTCTACCC	
	TAAGGGTCAC	AATTAGAAC	TCAGCGACTC	TTACTTGGAA	CACTTCAATG	AACAGATGGG	
	430	440	450	460	470	480	
SEQ01_ORF	*	*	*	*	*	*	*
	TCACACTGGA	CCCGGCTCCC	GGATATTCC	TGGGAGCTCG	GTCTCTGGT	CAGCCATTCA	
	AGTGTGACCT	GGGCCGAGGG	CCTATAAAGG	ACCCTCGAGC	CAGAGGACCA	GTCGGTAAGT	
	490	500	510	520	530	540	
SEQ01_ORF	*	*	*	*	*	*	*
	AGCTATTATT	TTGTTCCGGA	GCCCAGCGAC	CTTCAAAGTG	CAGTGAGCAT	CCTGGCTCTG	
	TCGATAATAA	AACAAGGCCT	CGGGTCGCTG	GAAGTTTCAC	GTCACTCGTA	GGACCGAGAC	
	550	560	570	580	590	600	
SEQ01_ORF	*	*	*	*	*	*	*
	ACCCCACAGA	GCAATGGAC	TTGACTTGC	GTGGCTACCT	GGAAGAGCCT	GAAGGCCCGC	
	TGGGGTGTCT	CGTTACCTG	AAACTGAACG	CACCGATGGA	CCTTCTCGGA	CTTCCGGGCG	
	610	620	630	640	650	660	
SEQ01_ORF	*	*	*	*	*	*	*
	AAGTCTGCAA	CTGTAAATCT	CACTGTGATT	CGGTGTCCCC	AAGACACTGG	AGGTGGTATT	
	TTCAGACGTT	GACATTAGA	GTGACACTAA	GCCACAGGGG	TTCTGTGACC	TCCACCATAA	
	670	680	690	700	710	720	
SEQ01_ORF	*	*	*	*	*	*	*
	AATATTCCAG	GTGTATTATC	AAGTTTACCG	AGTTTAGGT	TTTCATTGCC	TACTTGGGGC	
	TTATAAGGTC	CACATAATAG	TTCAAATGGC	TCAAATCCAA	AAAGTAACGG	ATGAACCCCG	
	730	740	750	760	770	780	
SEQ01_ORF	*	*	*	*	*	*	*
	AAAGTTGGAC	TTGGACTAGC	AGGCACCATG	CTTCTGACGC	CGACGTGTAC	TCTTACAATA	
	TTTCAACCTG	AACCTGATCG	TCCGTGGTAC	GAAGACTGCG	GCTGCACATG	AGAATGTTAT	
	790	800	810	820	830	840	
SEQ01_ORF	*	*	*	*	*	*	*
	CGCTGCTGCT	GCTGCCGCCG	TCGTTGTTGT	GGCTGCAACT	GCTGCTGCCG	TTGTTGTTTC	
	GCGACGACGA	CGACGGCGGC	AGCAACAACA	CCGACGTTGA	CGACGACGGC	AAACACAAAG	
	850	860	870	880	890	900	
SEQ01_ORF	*	*	*	*	*	*	*
	TGCTGTAGAA	GAAAAAGAGG	ATTCGTATT	CAATTCAA	AGAAATCTGA	AAAAGAGAAG	
	ACGACATCTT	CTTTTCTCC	TAAAGCATAA	GTAAAGTTT	TCTTAGACT	TTTTCTCTTC	

	910	920	930	940	950	960
SEQ01_ORF	ACAAACAAAG	AAACTGAGAC	AGAAAGTGG	AATGAAAAC	CCGGCTACAA	TTCAGATGAA
	TGTTTGTTC	TTTGACTCTG	TCTTCACCT	TTACTTTGA	GGCGATGTT	AAGTCTACTT
	970	980	990	1000	1010	1020
SEQ01_ORF	CAAAAGACCA	CAGACACCGC	TTCTCTCCCT	CCCAAATCCT	GTGAATCCAG	TGATCCTGAA
	GTTTTCTGGT	GTCTGTGGCG	AAGAGAGGGA	GGGTTTAGGA	CACTTAGGTC	ACTAGGACTT
	1030	1040	1050	1060	1070	1080
SEQ01_ORF	CAAAGAAACA	GTAGCTGTGG	CCCTCCTCAC	CAGCGGGCTG	ATCAACGTCC	ACCCAGGCCA
	GTTCCTTTGT	CATCGACACC	GGGAGGAGTG	GTCGCCCGAC	TAGTTGCAGG	TGGGTCCGGT
	1090	1100	1110	1120	1130	1140
SEQ01_ORF	GCAAGTCATC	CACAGGCTTC	TTTTAATCTG	GCCAGTCCTG	AGAAGGTCAG	TAATACAACT
	CGTTCAGTAG	GTGTCCGAAG	AAAATTAGAC	CGGTCAGGAC	TCTTCCAGTC	ATTATGTTGA
	*					
SEQ01_ORF	GTAGTA					
	CATCAT					

EXHIBIT B

	10	20	30	40	50	60	
	*	*	*	*	*	*	
SEQ03_ORF	ATGGTGGCAG	GAGCCATGGA	AAATAGAGAC	CCACCCGGTT	CTGGGTCTGG	TAATGAAGTC	
	TACCACCGTC	CTCGGTACCT	TTTATCTCTG	GGTGGGCCAA	GACCCAGACC	ATTACTTCAG	
	260	270	280	290	300		
Marra EST	gTGcTG--gt	cAtC-cTG--	-gc-tcA-gC	tg-aCaGcTT	CcGGaTCcaG	TtATcAgaTC>	
SEQ03_ORF	ATGGTGGCAG	GAGCCATGGA	AAATAGAGAC	CCACCCGGTT	CTGGGTCTGG	TAATGAAGTC	
	70	80	90	100	110	120	
	*	*	*	*	*	*	
SEQ03_ORF	ATAGAAGGCC	CCCAAAATGC	AAGAGTCCTG	AAGGGCTCCC	AGGCTCGCTT	CAACTGCACC	
	TATCTTCCGG	GGGTTTTACG	TTCTCAGGAC	TTCCCAGGG	TCCGAGCGAA	GTGACGTGG	
	310	320	330	340	350	360	
Marra EST	ATAGAAGGtC	CtCAgAATGt	AAcAGTCCTa	AAGGaCTCag	AGGCTCaTT	CAACTGCACC>	
SEQ03_ORF	ATAGAAGGCC	CCCAAAATGC	AAGAGTCCTG	AAGGGCTCCC	AGGCTCGCTT	CAACTGCACC	
	130	140	150	160	170	180	
	*	*	*	*	*	*	
SEQ03_ORF	GTCTCCCAGG	GCTGGAAGCT	CATCATGTGG	GCTCTCAGTG	ACATGGTGGT	GCTAAGCGTC	
	CAGAGGGTCC	CGACCTTCGA	GTAGTACACC	CGAGAGTCAC	TGTACCACCA	CGATTCGCAG	
	370	380	390	400	410	420	
Marra EST	GTgaCtCACG	GCTGGAAGCT	tcTCATGTGG	aCTCTtAacc	AaATGGTGGT	GCTgAGtcTC>	
SEQ03_ORF	GTCTCCCAGG	GCTGGAAGCT	CATCATGTGG	GCTCTCAGTG	ACATGGTGGT	GCTAAGCGTC	
	190	200	210	220	230	240	
	*	*	*	*	*	*	
SEQ03_ORF	AGGCCCATGG	AGCCCATCAT	CACCAATGAC	CGCTTCACCT	CTCAGAGGTA	CGACCAGGGC	
	TCCGGGTACC	TCGGGTAGTA	GTGGTTACTG	GCGAAGTGG	GAGTCTCCAT	GCTGGTCCCG	
	430	440	450	460	470	480	
Marra EST	ccaCCCAGG	-aCCCATCAT	CACCAAcaAC	CGtTTCACCT	aTgccAGtTA	-cAaCAGcat>	
SEQ03_ORF	AGGCCCATGG	AGCCCATCAT	CACCAATGAC	CGCTTCACCT	CTCAGAGGTA	CGACCAGGGC	
	250	260	270	280	290	300	
	*	*	*	*	*	*	
SEQ03_ORF	GGGAACATTCA	CCTCGGAGAT	GATCATCCAC	AATGTGGAGC	CCAGTGATTC	GGGAAACATC	
	CCCTTGAAGT	GGAGCCTCTA	CTAGTAGGTG	TTACACCTCG	GGTCACTAAG	CCCCTTGTAG	
	490	500	510	520			
Marra EST	GacAgCTTCA	tCTCGGAGtT	GATCATCCAt	gATGTGcAGC	CCAGTG>		
SEQ03_ORF	GGGAACATTCA	CCTCGGAGAT	GATCATCCAC	AATGTGGAGC	CCAGTG		

	310	320	330	340	350	360
SEQ03_ORF	*	*	*	*	*	*
	AGATGCAGCC	TCCAGAACAG	TCGCCTGCAT	GGATCTGCTT	ACCTTACCGT	CCAAGTTATG
	TCTACGTCGG	AGGTCTTGTG	AGCGGACGTA	CCTAGACGAA	TGGAATGGCA	GGTCAATAAC
	370	380	390	400	410	420
SEQ03_ORF	*	*	*	*	*	*
	GGAGAGCTGT	TCATTCCCAG	TGTTAATCTT	GTAGTCGCTG	AGAATGAACC	TTGTGAAGTT
	CCTCTCGACA	AGTAAGGTC	ACAATTAGAA	CATCAGCGAC	TCTTACTTGG	AACACTTCAA
	430	440	450	460	470	480
SEQ03_ORF	*	*	*	*	*	*
	ACTTGTCCTAC	CCTCACACTG	GACCTGGCTC	CCGGATATTTC	CCTGGGAGCT	CGGTCTCCTG
	TGAACAGATG	GGAGTGTGAC	CTGGACCGAG	GGCCTATAAA	GGACCCCTCGA	GCCAGAGGAC
	490	500	510	520	530	540
SEQ03_ORF	*	*	*	*	*	*
	GTCAGGCCATT	CAAGCTATTA	TTTTGTTCCG	GAGCCCAGCG	ACCTTCAAAG	TGCACTGAGC
	CAGTCGGTAA	GTTCGATAAT	AAAACAAGGC	CTCGGGTCGC	TGGAAGTTTC	ACGTCACTCG
	550	560	570	580	590	600
SEQ03_ORF	*	*	*	*	*	*
	ATCCTGGCTC	TGACCCACA	GAGCAATGGG	ACTTIGACTT	GCGTGGCTAC	CTGGAAGAGC
	TAGGACCGAG	ACTGGGGTGT	CTCGTTACCC	TGAAACTGAA	CGCACCGATG	GACCTTCTCG
	610	620	630	640	650	660
SEQ03_ORF	*	*	*	*	*	*
	CTGAAGGCC	GCAAGTCTGC	AACTGTAAAT	CTCACTGTGA	TTCGGTGTCC	CCAAGACACT
	GACTTCCGGG	CGTTCAGACG	TTGACATTAA	GAGTGACACT	AAGCCACAGG	GGTTCTGTGA
	670	680	690	700	710	720
SEQ03_ORF	*	*	*	*	*	*
	GGAGGGGGTA	TTAATATTCC	AGGTGTATTA	TCAAGTTTAC	CGAGTTTAGG	TTTTTCATTG
	CCTCCACCAT	AATTATAAGG	TCCACATAAT	AGTTCAAATG	GCTCAAATCC	AAAAAGTAAC
	730	740	750	760	770	780
SEQ03_ORF	*	*	*	*	*	*
	CCTACTTGGG	GCAAAGTTGG	ACTTGGACTA	GCAGGCCACCA	TGCTTCTGAC	GCCGACGTGT
	GGATGAACCC	CGTTTCAACC	TGAACCTGAT	CGTCCGTGGT	ACGAAGACTG	CGGCTGCACA
	790	800	810	820	830	840
SEQ03_ORF	*	*	*	*	*	*
	ACTCTTACAA	TACGCTGCTG	CTGCTGCCGC	CGTCGTTGTT	GTGGCTGCAA	CTGCTGCTGC
	TGAGAATGTT	ATGCGACGAC	GACGACGGCG	GCAGCAACAA	CACCGACGTT	GACGACGACG
	850	860	870	880	890	900
SEQ03_ORF	*	*	*	*	*	*
	CGTTGTTGTT	TCTGCTGTAG	AAGAAAAAGA	GGATTCGTA	TTCAATTCA	AAAGAAATCT
	GCAACAACAA	AGACGACATC	TTCTTTTCT	CCTAAAGCAT	AAGTTAAAGT	TTTCTTTAGA

910 * * 920 * * 930 * * 940 * * 950 * * 960 * *
SEQ03_ORF GAAAAAGAGA AGACAAACAA AGAAACTGAG ACAGAAAGTG GAAATGAAAA CTCCGGCTAC
CTTTTCTCT TCTGTTTGTT TCTTGACTC TGTCTTCAC CTTTACTTT GAGGCCGATG

970 * * 980 * * 990 * * 1000 * * 1010 * * 1020 * *
SEQ03_ORF AATTCAAGATG AACAAAAGAC CACAGACACC GCTTCTCTCC CTCCCAAATC CTGTGAATCC
TTAAGTCTAC TTGTTTCTG GTGTCTGTGG CGAAGAGAGG GAGGGTTAG GACACTTAGG

1030 * * 1040 * * 1050 * * 1060 * * 1070 * * 1080 * *
SEQ03_ORF AGTGATCCTG AACAAAGAAA CAGTAGCTGT GGCCCTCCTC ACCAGCGGGC TGATCAACGT
TCACTAGGAC TTGTTCTTT GTCATCGACA CGGGGAGGAG TGGTCGCCCCG ACTAGTTGCA

1090 * * 1100 * * 1110 * * 1120 * * 1130 * * 1140 * *
SEQ03_ORF CCACCCAGGC CAGCAAGTCA TCCACAGGCT TCTTTTAATC TGGCCAGTCC TGAGAAGGTC
GGTGGGTCCG GTCGTTCAGT AGGTGTCCGA AGAAAATTAG ACCGGTCAGG ACTCTTCCAG

1150 * * *
SEQ03_ORF AGTAATACAA CTGTAGTA
TCATTATGTT GACATCAT

EXHIBIT C

	10	20	30	40	50	60	
	*	*	*	*	*	*	*
SEQ05_ORF	ATGGAAAGGC	ATTTGCTCAC	GGTCCAGAA	GCTGTAGGTT	CTGGGTCTGG	TAATGAAGTC	
	TACCTTTCCG	TAAACGAGTG	CCAAGGTCTT	CGACATCCAA	GACCCAGACC	ATTACTTCAG	
	250	260	270	280	290	300	
Marra EST	cTGGctgtGC	tggTcaTCct	GGc-tCAGct	--gacAGcTT	CcGGaTCcaG	TtATcAgaTC>	
SEQ05_ORF	ATGGAAAGGC	ATTTGCTCAC	GGTCCAGAA	GCTGTAGGTT	CTGGGTCTGG	TAATGAAGTC	
	70	80	90	100	110	120	
	*	*	*	*	*	*	*
SEQ05_ORF	ATAGAAGGCC	CCCAGAAATGC	AACAGTCCTG	AAGGGCTCCC	AGGCTCGCTT	CAACTGCACC	
	TATCTTCCGG	GGGTCTTACG	TTGTCAGGAC	TTCCCGAGGG	TCCGAGCGAA	GTTGACGTGG	
	310	320	330	340	350	360	
Marra EST	ATAGAAGGtC	CtCAGAAATGt	AACAGTCCTa	AAGGaCTCag	AGGCTCaCTT	CAACTGCACC>	
SEQ05_ORF	ATAGAAGGCC	CCCAGAAATGC	AACAGTCCTG	AAGGGCTCCC	AGGCTCGCTT	CAACTGCACC	
	130	140	150	160	170	180	
	*	*	*	*	*	*	*
SEQ05_ORF	GTCTCCCAGG	GCTGGAAGCT	CATCATGTGG	GCTCTCAGTG	ACATGGTGGT	GCTAAGCGTC	
	CAGAGGGTCC	CGACCTTCGA	GTAGTACACC	CGAGAGTCAC	TGTACCACCA	CGATTCGCAG	
	370	380	390	400	410	420	
Marra EST	GTgaCtCAcG	GCTGGAAGCT	tcTCATGTGG	aCTCTtAacc	AaATGGTGGT	GCTgAGtcTC>	
SEQ05_ORF	GTCTCCCAGG	GCTGGAAGCT	CATCATGTGG	GCTCTCAGTG	ACATGGTGGT	GCTAAGCGTC	
	190	200	210	220	230	240	
	*	*	*	*	*	*	*
SEQ05_ORF	AGGCCCATGG	AGCCCATCAT	CACCAATGAC	CGCTTCACCT	CTCAGAGGTA	CGACCAGGGC	
	TCCGGGTACC	TCGGGTAGTA	GTGGTTACTG	GCGAAGTGGA	GAGTCTCCAT	GCTGGTCCCG	
	430	440	450	460	470	480	
Marra EST	ccaCCCaaGG	-aCCCATCAT	CACCAAAcAC	CGtTTCACCT	aTgccAGtTA	-cAaCAGcat>	
SEQ05_ORF	AGGCCCATGG	AGCCCATCAT	CACCAATGAC	CGCTTCACCT	CTCAGAGGTA	CGACCAGGGC	
	250	260	270	280	290	300	
	*	*	*	*	*	*	*
SEQ05_ORF	GGGAACTTCA	CCTCGGAGAT	GATCATCCAC	AATGTGGAGC	CCAGTGATTC	GGGGAACATC	
	CCCTTGAAGT	GGAGCCTCTA	CTAGTAGGTG	TTACACCTCG	GGTCACTAAG	CCCCTTGTAG	
	490	500	510	520			
Marra EST	GacAgCTTCA	tCTCGGAGtT	GATCATCCAT	gATGTGcAGC	CCAGTG>		
SEQ05_ORF	GGGAACTTCA	CCTCGGAGAT	GATCATCCAC	AATGTGGAGC	CCAGTG		

SEQ05_ORF	310	320	330	340	350	360
	*	*	*	*	*	*
	AGATGCAGCC	TCCAGAACAG	TCGCCTGCAT	GGATCTGCTT	ACCTTACCGT	CCAAGTTATG
	TCTACGTCGG	AGGTCTTGTC	AGCGGACGTA	CCTAGACGAA	TGGAATGGCA	GGTTCAATAC
SEQ05_ORF	370	380	390	400	410	420
	*	*	*	*	*	*
	GGAGAGCTGT	TCATTCCCAG	TGTTAATCTT	GTAGTCGCTG	AGAATGAACC	TTGTGAAGTT
	CCTCTCGACA	AGTAAGGGTC	ACAATTAGAA	CATCAGCGAC	TCTTACTTGG	AACACTTCAA
SEQ05_ORF	430	440	450	460	470	480
	*	*	*	*	*	*
	ACTTGTCTAC	CCTCACACTG	GACCCGGCTC	CCGGATATT	CCTGGGAGCT	CGGTCTCCTG
	TGAACAGATG	GGAGTGTGAC	CTGGGCCGAG	GGCCTATAAA	GGACCCTCGA	GCCAGAGGAC
SEQ05_ORF	490	500	510	520	530	540
	*	*	*	*	*	*
	GTCAGCCATT	CAAGCTATT	TTTGTTCG	GAGCCCAGCG	ACCTTCAAAG	TGCA
	CAGTCGGTAA	GTTCGATAAT	AAAACAAGGC	CTCGGGTCG	TGGAAGTTTC	ACGTCACTCG
SEQ05_ORF	550	560	570	580	590	600
	*	*	*	*	*	*
	ATCCTGGCTC	TGACCCCACA	GAGCAATGGG	ACTTTGACTT	CGTGGCTAC	CTGGAAGAGC
	TAGGACCGAG	ACTGGGGTGT	CTCGTTACCC	TGAAACTGAA	CGCACCGATG	GACCTTCTCG
SEQ05_ORF	610	620	630	640	650	660
	*	*	*	*	*	*
	CTGAAGGCC	GCAAGTCTGC	AACTGTAAAT	CTCACTGTGA	TTCGGTGTCC	CCAAGACACT
	GACTTCCGGG	CGTTCAGACG	TTGACATT	GAGTGACACT	AAGCCACAGG	GGTTCTGTGA
SEQ05_ORF	670	680	690	700	710	720
	*	*	*	*	*	*
	GGAGGGGGTA	TTAATATTCC	AGGTGTATTA	TCAAGTTAC	CGAGTTAGG	TTTTTCATTG
	CCTCCACCAT	AATTATAAGG	TCCACATAAT	AGTTCAAATG	GCTCAAATCC	AAAAAGTAAC
SEQ05_ORF	730	740	750	760	770	780
	*	*	*	*	*	*
	CCTACTTGGG	GCAAAGTTGG	ACTTGGACTA	GCAGGCCACCA	TGCTTCTGAC	GCCGACGTGT
	GGATGAACCC	CGTTCAACC	TGAACCTGAT	CGTCCGTGGT	ACGAAGACTG	CGGCTGCACA
SEQ05_ORF	790	800	810	820	830	840
	*	*	*	*	*	*
	ACTCTTACAA	TACGCTGCTG	CTGCTGCCGC	CGTCGTTGTT	GTGGCTGCAA	CTGCTGCTGC
	TGAGAAATGTT	ATGCGACGAC	GACGACGGCG	GCAGCAACAA	CACCGACGTT	GACGACGACG
SEQ05_ORF	850	860	870	880	890	900
	*	*	*	*	*	*
	CGTTGTTGTT	TCTGCTGTAG	AAGAAAAAGA	GGATTTGTA	TTCAATTCA	AAAGAAATCT
	GCAACAACAA	AGACGACATC	TTCTTTTCT	CCTAAAGCAT	AAGTTAAAGT	TTTCTTTAGA

	910	920	930	940	950	960	
SEQ05_ORF	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	
	GAAAAAGAGA	AGACAAACAA	AGAAACTGAG	ACAGAAAGTG	GAAATGAAAA	CTCCGGCTAC	
	CTTTTCTCT	TCTGTTGTT	TCTTGACTC	TGTCTTCAC	CTTTACTTTT	GAGGCCGATG	
	970	980	990	1000	1010	1020	
SEQ05_ORF	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	
	AATTCAAGATG	AACAAAAGAC	CACAGAAACC	GCTTCTCTCC	CTCCCCAAATC	CTGTGAATCC	
	TTAAGTCTAC	TTGTTTCTG	GTGTCTTG	CGAAGAGAGG	GAGGGTTAG	GACACTTAGG	
	1030	1040	1050	1060	1070	1080	
SEQ05'_ORF	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	
	AGTGATCCCTG	AACAAAGAAA	CAGTAGCTGT	GGCCCTCCTC	ACCAGCGGGC	TGATCAACGT	
	TCACTAGGAC	TTGTTTCTTT	GTCATCGACA	CCGGGAGGAG	TGGTCGCCCG	ACTAGTTGCA	
	1090	1100	1110	1120	1130	1140	
SEQ05_ORF	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	
	CCACCCAGGC	CAGCAAGTCA	TCCACAGGCT	TCTTTTAATC	TGGCCAGTCC	TGAGAAGGTC	
	GGTGGGTCCG	GTCGTTCAGT	AGGTGTCCGA	AGAAAATTAG	ACCGGTCAAGG	ACTCTTCCAG	
	1150						
SEQ05_ORF	* * * *						
	AGTAATACAA	CTGTAGTA					
	TCATTATGTT	GACATCAT					

EXHIBIT D

44210 44220 44230 44240 44250
AF121782 AGAAAGGTTACAGCACACAGTTGATTATGGAGATCCATTAAACAA
TCTTTCCAATGTCGTGTCAACTAAATACCTCTAGGTAAGTAAATTGTT

44260 44270 44280 44290 44300
AF121782 CTTGAAAAATTGGCTACCTTCCAGGTTCTGGGCTGGTAATGAAGTCATA
GAACTTTAACCGATGGAAGGTCCAAGACCCAGACCATTACTTCAGTAT

1. SEQ01_ORF 10 20 30 40 50
[1598] CTTG--TGATT---TTCCTCCACGGTTCTGGGCTGGTAATGAAGTCATA>
||||| |||| | ||| | |||||||||||||||||||||||
AF121782 CTTGAAAAATTGGCTACCTTCCAGGTTCTGGGCTGGTAATGAAGTCATA

44310 44320 44330 44340 44350
AF121782 GAAGGCCCCAAAATGCAAGAGTCCTGAAGGGCTCCCAGGCTCGCTCAA
CTTCCGGGGTTTACGTTCTCAGGACTCCGAGGGTCCGAGCGAAGTT

1. SEQ01_ORF 60 70 80 90 100
[1598] GAAGGCCCCAGAATGCAACACAGTCCTGAAGGGCTCCCAGGCTCGCTCAA>
||||| ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
AF121782 GAAGGCCCCAAAATGCAAGAGTCCTGAAGGGCTCCCAGGCTCGCTCAA

44360 44370 44380 44390 44400
AF121782 CTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGCTCTCAGTGACA
GACGTGGCAGAGGTCCGACCTCGAGTAGTACACCCGAGAGTCACTGT

1. SEQ01_ORF 110 120 130 140 150
[1598] CTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGCTCTCAGTGACA>
||||| ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
AF121782 CTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGCTCTCAGTGACA

44410 44420 44430 44440 44450
AF121782 TGGTGGTGCTAACCGTCAGGCCATGGAGGCCATCATACCAATGACCGC
ACCACCAACGATTGCACTCGAGTCGGTAGCTCGGGTAGTAGTGGTTACTGGCG

1. SEQ01_ORF 160 170 180 190 200
[1598] TGGTGGTGCTAACCGTCAGGCCATGGAGGCCATCATACCAATGACCGC>
||||| ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
AF121782 TGGTGGTGCTAACCGTCAGGCCATGGAGGCCATCATACCAATGACCGC

44460 44470 44480 44490 44500
AF121782 TTCACCTCTCAGAGGTACGACCAGGGGGAACTTCACCTCGGAGATGAT
AAGTGGAGAGTCCTCATGCTGGTCCGCCCTGAAGTGGAGCCTACTA

1. SEQ01_ORF 210 220 230 240 250
[1598] TTCACCTCTCAGAGGTACGACCAGGGGGAACTTCACCTCGGAGATGAT>
||||| ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
AF121782 TTCACCTCTCAGAGGTACGACCAGGGGGAACTTCACCTCGGAGATGAT

	44510	44520	44530	44540	44550
AF121782	CATCCACAATGTGGAGCCCAGTGATTGGGGAACATCAGATGCAGCCTCC				
	GTAGGTGTTACACCTCGGGTCACTAAGCCCCTGTAGTCTACGTCGGAGG				
1. SEQ01_ORF	260	270	280	290	300
[1598]	CATCCACAATGTGGAGCCCAGTGATTGGGGAACATCAGATGCAGCCTCC>				
AF121782	CATCCACAATGTGGAGCCCAGTGATTGGGGAACATCAGATGCAGCCTCC				
	44560	44570	44580	44590	44600
AF121782	AGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAAGGTGTAT				
	TCTTGTCAAGCGGACGTACCTAGACGAATGGAATGGCAGGTTCCACACATA				
1. SEQ01_ORF	310	320	330	340	
[1598]	AGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCA-GT-T--AT>				
AF121782	AGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAAGGTGTAT				
	44610	44620	44630	44640	44650
AF121782	GCAGGTGGCTTCTGAAGTCATCAGGTTAAATGTCAGAGGGCAGGAAGGA				
	CGTCCACCGAAGACTTCAGGTAGTCCAATTACAGTCTCCGTCTTCCT				
		T	TC		
1. SEQ01_ORF	350	360	370	380	390
[1598]	G--GGAGAGCTGTTCATTC--CAGGTTAAATTGTTAGTCGCTGAGAATGAA>				
AF121782	GCAGGTGGCTTCTGAAGTCATCAGGTTAAATGTCAGAGGGCAGGAAGGA				
	44660	44670	44680	44690	44700
AF121782	CCTTCTAAAGTTCATGCCCGTATGATGGCAGACGTGGCTACCTTCAGT				
	GGAAGATTCAAGTACGGCGATACTACCGTCTGCACCAGATGGAAGTCA				
		A		G	
1. SEQ01_ORF	400	410	420	430	440
[1598]	CCTTGTGAAGTTCTTGTCTACCCCTCACACTGGACCCGG-CTCCCGATATT>				
AF121782	CCTTCTAAAGTTCATGCCCGTATGATGGCAGACGTGGCTACCTTCAGT				
	44710	44720	44730	44740	44750
AF121782	TGGTGTGACCTACAATTATTCTGAACGTGATGAATGTTGCGATTATT				
	ACCACAACTGGATGTTAATAAGACTTGACTACTACAAAACGCTAAATAA				
			CC		
1. SEQ01_ORF	450	460	470	480	490
[1598]	TCCTG-GGAGCT-C-GGTCTCCTGGTCAGATTCAAGCTAT--TATTGTTGT>				
AF121782	TGGTGTGACCTACAATTATTCTGAACGTGATGAATGTTGCGATTATT				

44760 44770 44780 44790 44800
AF121782 TGTCGCCTCCTTCCTCCCTCATGCTCTCCCTACCTCCTCACTTCTTCTTC
ACAGCGGAGGAAGGAGGGAGTACGAGAGGATGGAGGAGTGAAGAAGAAG

A
1. SEQ01_ORF 500 510 | 520 530 540
[1598] TCCGGAGCCCAGCGACCTTCAAGTGCAGTGAGCATCCTGGCTCTGACCCCC>
AF121782 TGTCGCCTCCTTCCTCCCTCATGCTCTCCCTACCTCCTCACTTCTTCTTC

44810 44820 44830 44840 44850
AF121782 CCTTCTCCCCCTCTTCCTTCCTGTGTGCTCTAGCCTTCAGTTGGCAAT
GGAAGAGGGGGAGAGAAGGAAGGACACACGAGATCGGAAGTCAAACCGTTA

1. SEQ01_ORF 550 560 570 580 590
[1598] ACAGAGCAATGGGACTT-TGACTTGCCTG-GCTA-CCTGGAAGAGCCTGA>
AF121782 CCTTCTCCCCCTCTTCCTTCCTGTGTGCTCTAGCCTTCAGTTGGCAAT

44860 44870 44880 44890 44900
AF121782 AGGCTTAGAATTATTCTGGATGGACTAATGTTATTGTTTCGTTGATTAA
TCCGAATCTTAATAAGACCTACCTGATTACAAATAACAAAGCAACTAAAT

G TCCCCA
1. SEQ01_ORF 600 610 620 | 630 |
[1598] AGGC-CCGCA--AGTCTGCAACTGTAAATCTCACTTGATTGGTGGAGACA>
AF121782 AGGCTTAGAATTATTCTGGATGGACTAATGTTATTGTTTCGTTGATTAA

44910 44920 44930 44940 44950
AF121782 TCCCCCTCTTCCTCACTTCCTCCATCTTCCCTTTCTGCTTCATT
AGGGGGAAGAAGGAGTGAAGGAGGGTAGAAAGGGAAAAAGGACGAAGTAA

T
1. SEQ01_ORF 650 660 | 670 680 690
[1598] CTGGAGGTGGTATTAAATTCCAGGTGTATTATCAAGTTACCGAGT--TT>
AF121782 TCCCCCTCTTCCTCACTTCCTCCATCTTCCCTTTCTGCTTCATT

44960 44970 44980 44990 45000
AF121782 CTCTTTCTCCTTCCATCTTGCTTCTCCCTTTCTGGTTAAGACTGATAG
GAGAAAGAGGAAGGTAGAAACGAAAGGAAAAAGACCAATTCTGACTATC

1. SEQ01_ORF 700 710 720 730 740
[1598] AGGTTTTCATGCCTACTTG--GGGAAAGTTGGACTT-GGACTAGCAG>
AF121782 CTCTTTCTCCTTCCATCTTGCTTCTCCCTTTCTGGTTAAGACTGATAG

	45260	45270	45280	45290	45300
AF121782	ACCTGCCTCCAACACTACAGTGGGATAGTCATTATAGTCAGTCAAAGTTGTGTGT				
	TGGGACGGAGGTTGATGTCACCCTATCAGTAATATCAGTTCAACACACA				
	A				
	AGC GCC				
1. SEQ01_ORF	1000	1010	1020	1030	
[1598]	CCCAATCCTGTGAATCCAGT--GATCCTGAACAAAGAAACAGTTGTCTCC>				
AF121782	ACCTGCCTCCAACACTACAGTGGGATAGTCATTATAGTCAGTCAAAGTTGTGTGT				
	45310	45320	45330	45340	45350
AF121782	TCACCAAATATATCAAGTCATTGAGAGAAAAGAAAAGAATAAACAAAATT				
	AGTGGTTTATATAGTCAGTAACTCTTTCTTTCTTATTGTTAA				
	GCG				
	C				
1. SEQ01_ORF1050	1060	1070	1080	1090	
[1598]	TCACCAAGGCTGATCAAGTC-CACCCAGGCCAGCAAGTCATCCAC-AGGCT>				
AF121782	TCACCAAATATATCAAGTCATTGAGAGAAAAGAAAAGAATAAACAAAATT				
	45360	45370	45380	45390	45400
AF121782	TATAATAATAGCTTATTTTCATTTAGAGGTAATTGGAGGTGCTGAAG				
	ATATTATTATCGAATAAAAGTAAACCTCCATTAAACCTCCACGACTTC				
1. SEQ01_O1100	1110	1120	1130	1140	
[1598]	TCTTTAAT--CTGGCCAGTCCTGAGA-AGGTCAGTAATA-CAACTGTAG>				
AF121782	TATAATAATAGCTTATTTTCATTTAGAGGTAATTGGAGGTGCTGAAG				
	45410	45420	45430	45440	45450
AF121782	ATAATGTTACACAGTAAAAAGTAAAGGATGCTTACAAAGATTGGAA				
	TATTACAATGTGTCATTTTCATTTCTACGAAATGTTCTAACCTT				
1. SEQ01_ORF					
[1598]	-TA>				
AF121782	ATA				
	45460	45470	45480	45490	45500
AF121782	TAGTCTTACCAAAATTAAATCAGTTGCATTCTTAAAGTGTATTATA				
	ATCAGAATGGTTAAATTAGTGAAACGTAAGAAATTTCACATAAATAT				

EXHIBIT E

	44510	44520	44530	44540	44550
AF121782	CATCCACAATGTGGAGCCCAGTGATTGGGGAACATCAGATGCAGCCTCC				
	GTAGGTGTTACACCTCGGGTCACTAAGCCCCTGTAGTCTACGTCGGAGG				
1. SEQ03_ORF	270	280	290	300	310
[1636]	CATCCACAATGTGGAGCCCAGTGATTGGGGAACATCAGATGCAGCCTCC>				
AF121782	CATCCACAATGTGGAGCCCAGTGATTGGGGAACATCAGATGCAGCCTCC				
	44560	44570	44580	44590	44600
AF121782	AGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAAGGTGTAT				
	TCTTGTCAAGCGGACGTACCTAGACGAATGGAATGGCAGGTTCCACACATA				
1. SEQ03_ORF	320	330	340	350	
[1636]	AGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAAGGTGTAT>				
AF121782	AGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAAGGTGTAT				
	44610	44620	44630	44640	44650
AF121782	GCAGGTGGCTCTGAAGTCATCAGGTTAAATGTCAGAGGGCAGGAAGGA				
	CGTCCACCGAACACTCAGGTAGTCCAATTACAGTCTCCGTCTTCCT				
		T	TC		
1. SEQ03_O360	370	380	390	400	
[1636]	G--GGAGAGCTGTTCATTC--CAGGTTAAATTGAGTCGCTGAGAATGAA>				
AF121782	GCAGGTGGCTCTGAAGTCATCAGGTTAAATGTCAGAGGGCAGGAAGGA				
	44660	44670	44680	44690	44700
AF121782	CCTTCTAAAGTTCATGCCCGTATGATGGCAGACGTGGTCTACCTTCAGT				
	GGAAGATTCAAGTACGGCGCATACTACCGTCTGCACCAGATGGAAGTCA				
		A		G	
1. SEQ03_OR410	420	430	440	450	
[1636]	CCTTGTGAAGTTCTTGTCTACCCCTCACACTGGACCTGG-CTCCCGATATT>				
AF121782	CCTTCTAAAGTTCATGCCCGTATGATGGCAGACGTGGTCTACCTTCAGT				
	44710	44720	44730	44740	44750
AF121782	TGGTGGTGACCTACAATTATTCTGAACGTGATGAATGTTGCGATTATT				
	ACCACAACTGGATGTTAATAAGACTTGACTACTACAAAACGCTAAATAA				
		CC			
1. SEQ03_O460	470	480	490	500	
[1636]	TCCTG-GGAGCT-C-GGTCTCCTGGTCAGATTCAAGCTAT--TATTTGT>				
AF121782	TGGTGGTGACCTACAATTATTCTGAACGTGATGAATGTTGCGATTATT				

	44760	44770	44780	44790	44800
AF121782	TGTCGCCTCCTTCCTCCCTCATGCTCTCCCTACCTCCTCACTTCTTCTTC				
	ACAGCGGAGGAAGGAGGGAGTACGAGAGGGATGGAGGAGTGAAGAAGAAG				
	A				
1. SEQ03_ORF	510	520	530	540	550
[1636]	TCCGGAGCCCAGCGACCTCAAGTGCAGTGACATCCTGGCTCTGACCCCC>				
AF121782	TGTCGCCTCCTTCCTCCCTCATGCTCTCCCTACCTCCTCACTTCTTCTTC				
	44810	44820	44830	44840	44850
AF121782	CCTTCTCCCCCTCTTCCTTCCTGTGTGCTCTAGCCTTCAGTTGGCAAT				
	GGAAGAGGGGGAGAGAAGGAAGGACACACGAGATCGGAAGTCAACCGTTA				
1. SEQ03_ORF	560	570	580	590	600
[1636]	ACAGAGCAATGGGACTT-TGACTTGCCTG-GCTA-CCTGGAAGAGCCTGA>				
AF121782	CCTTCTCCCCCTCTTCCTTCCTGTGTGCTCTAGCCTTCAGTTGGCAAT				
	44860	44870	44880	44890	44900
AF121782	AGGCTTAGAATTATTCTGGATGGACTAATGTTATTGTTCTGTTGATTAA				
	TCCGAATCTTAATAAGACCTACCTGATTACAAATAACAAAGCAACTAAAT				
1. SEQ03_ORF	610	620	630	640	TCCCCA
[1636]	AGGC-CCGCA--AGTCTGCAACTGTAAATCTCACTTGATTGGTGGAGACA>				
AF121782	AGGCTTAGAATTATTCTGGATGGACTAATGTTATTGTTCTGTTGATTAA				
	44910	44920	44930	44940	44950
AF121782	TCCCCCTTCTCCTCACTTCCTCCATCTTCCCTTTCTGCTTCATT				
	AGGGGAAAGAAGGAGTGAAGGAGGGTAGAAAGGGAAAAAGGACGAAGTAA				
1. SEQ03_ORF660	670	680	690	700	T
[1636]	CTGGAGGTGGTATTAAATTCCAGGTGTATTATCAAGTTACCGAGT--TT>				
AF121782	TCCCCCTTCTCCTCACTTCCTCCATCTTCCCTTTCTGCTTCATT				
	44960	44970	44980	44990	45000
AF121782	CTCTTTCTCCTCCATCTTGCTTCTTCTGGTTAAGACTGATAG				
	GAGAAAGAGGAAGGTAGAAACGAAAGGAAAAAGACCAATTCTGACTATC				
1. SEQ03_ORF710	720	730	740	750	
[1636]	AGGTTTTCATTCGCTACTTG--GGGCAAAGTTGGACTT-GGACTAGCAG>				
AF121782	CTCTTTCTCCTCCATCTTGCTTCTTCTGGTTAAGACTGATAG				

45260	45270	45280	45290	45300	
AF121782	ACCTGCCTCCA ACTACAGTGGGATAGTCATTATAGTC TGGGACGGAGGTTGATGTCACCC TATCAGTAATATCAG TTCAACACACA				
	A		AGC	GGCC	
1. SEQ03_ORF	1010	1020	1030	1040	1050
[1636]	CCCAATCCTGTGAATCCAGT--GATCCTGAACAAAGAA ACAGTTGTCTCC>				
AF121782	ACCTGCCTCCA ACTACAGTGGGATAGTCATTATAGTC TGGGACGGAGGTTGATGTCACCC TATCAGTAATATCAG TTCAACACACA				
45310	45320	45330	45340	45350	
AF121782	TCACCAAATATATCAAGTCATTGAGAGAAAAGAAA AGAATAAACAAAATT				
	GCG	C			
1. SEQ03_O1060	1070	1080	1090	1100	1110
[1636]	TCACCAGGCTGATCAAGTC-CACCCAGGCCAGCAAGT CATCCAC-AGGCT>				
AF121782	TCACCAAATATATCAAGTCATTGAGAGAAAAGAAA AGAATAAACAAAATT				
45360	45370	45380	45390	45400	
AF121782	TATAATAATAGCTTATTTTCATTTAGAGGTAATTGGAG GTGCTGAAG				
1. SEQ03_ORF	1120	1130	1140	1150	
[1636]	TCTTTAAT--CTGGCCAGTCCTGAGA-AGGTCA GTAATA-CAACTGTAG>				
AF121782	TATAATAATAGCTTATTTTCATTTAGAGGTAATTGGAG GTGCTGAAG				
45410	45420	45430	45440	45450	
AF121782	ATAATGTTACACAGTAAAAAGTAAAAGGATGCTTAC AAAGATTGGAA				
1. SEQ03_ORF	-TA>				
[1636]					
AF121782	ATA				
45460	45470	45480	45490	45500	
AF121782	TAGTCTTACAAAATTAAATC ACTTTGCATTCTTAAAAGTGTATTATA ATCAGAACGTTAAATTAGTGA AAACGTAAGAAATTTCACATAAAATAT				

EXHIBIT F

	44460	44470	44480	44490	44500
AF121782	TTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGAT				
	AAGTGGAGAGTCTCCATGCTGGTCCGCCCTGAAGTGGAGCCTACTA				
1. SEQ05_ORF	220	230	240	250	260
[1596]	TTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGAT>				
AF121782	TTCACCTCTCAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGAT				
	44510	44520	44530	44540	44550
AF121782	CATCCACAATGTGGAGCCCAGTGATTGGGGAACATCAGATGCAGCCTCC				
	GTAGGTGTTACACCTCGGGTCACTAAGCCCCTGTAGTCTACGTCGGAGG				
1. SEQ05_ORF	270	280	290	300	310
[1596]	CATCCACAATGTGGAGCCCAGTGATTGGGGAACATCAGATGCAGCCTCC>				
AF121782	CATCCACAATGTGGAGCCCAGTGATTGGGGAACATCAGATGCAGCCTCC				
	44560	44570	44580	44590	44600
AF121782	AGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAAGGTGTAT				
	TCTTGTCAAGCGGACGTACCTAGACGAATGGAATGGCAGGTTCCACACATA				
1. SEQ05_ORF	320	330	340	350	
[1596]	AGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCA-GT-T--AT>				
AF121782	AGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAAGGTGTAT				
	44610	44620	44630	44640	44650
AF121782	GCAGGTGGCTCTGAAGTCATCAGGTTAAATGTCAGAGGGCAGGAAGGA				
	CGTCCACCGAAGACTTCAGTAGTCCAATTACAGTCTCCGTCTTCT				
1. SEQ05_O360			T	TC	
[1596]	370	380	390		400
AF121782	GCAGGTGGCTCTGAAGTCATCAGGTTAAATGTCAGAGGGCAGGAAGGA				
	44660	44670	44680	44690	44700
AF121782	CCTTCTAAAGTTCATGCCCGTATGATGGCAGACGTGGTCTACCTTCAGT				
	GGAAGATTCAAGTACGGCGCATACTACCGTCTGCACCAGATGGAAGTCA				
	A			G	
1. SEQ05_OR410	420	430	440	450	
[1596]	CCTTGTGAAGTTCTTGTCTACCTCACACTGGACCCGG-CTCCCGATATT>				
AF121782	CCTTCTAAAGTTCATGCCCGTATGATGGCAGACGTGGTCTACCTTCAGT				

44710 44720 44730 44740 44750
AF121782 TGGTGTGACCTACAATTATTCTGAACTGATGAATGTTTGCATTATT
ACCACAACTGGATGTTAATAAGACTTACACTTACAAAACGCTAAATAA

CC
|
1. SEQ05_O460 470 480 490 500
[1596] TCCTG-GGAGCT-C-GGTCTCCTGGTCAGATTCAAGCTAT--TATTTTGT>
AF121782 TGGTGTGACCTACAATTATTCTGAACTGATGAATGTTTGCATTATT

44760 44770 44780 44790 44800
AF121782 TGTCGCCTCCTTCCTCCCTCATGCTCTCCCTACCTCCTCACTTCTTCTTC
ACAGCGGAGGAAGGAGGGAGTACGAGAGGGATGGAGGAGTGAAGAAGAAG

A
|
1. SEQ05_ORF 510 520 530 540 550
[1596] TCCGGAGCCCAGCGACCTCAAGTGCAGTGAGCATCCTGGCTCTGACCCC>
AF121782 TGTCGCCTCCTTCCTCCCTCATGCTCTCCCTACCTCCTCACTTCTTCTTC

44810 44820 44830 44840 44850
AF121782 CCTTCTCCCCCTCTTCCTTCCTGTGTGCTCTAGCCTTCAGTTGGCAAT
GGAAGAGGGGGAGAGAAGGAAGGACACACGAGATCGGAAGTCAACCGTTA

1. SEQ05_ORF560 570 580 590 600
[1596] ACAGAGCAATGGGACTT-TGACTTGCCTG-GCTA-CCTGGAAGAGCCTGA>
AF121782 CCTTCTCCCCCTCTTCCTTCCTGTGTGCTCTAGCCTTCAGTTGGCAAT

44860 44870 44880 44890 44900
AF121782 AGGCTTAGAATTATTCTGGATGGACTAATGTTATTGTTTCGTTGATTAA
TCCGAATCTAATAAGACCTACCTGATTACAAATAACAAAGCAACTAAAT

G TCCCCA
| |
1. SEQ05_ORF 610 620 630 640
[1596] AGGC-CCGCA--AGTCTGCAACTGTAAATCTCACTTGATTGGTGGAGACA>
AF121782 AGGCTTAGAATTATTCTGGATGGACTAATGTTATTGTTTCGTTGATTAA

44910 44920 44930 44940 44950
AF121782 TCCCCCTTCCTCACTTCCTCCCATCTTCCCTTTCCCTGCTTCATT
AGGGGAAAGAAGGAGTGAAGGAGGGTAGAAAGGAAAAAGGACGAAGTAA

T
|
1. SEQ05_ORF660 670 680 690 700
[1596] CTGGAGGTGGTATTAAATTCCAGGTGTATTATCAAGTTACCGAGT--TT>
AF121782 TCCCCCTTCCTCACTTCCTCCCATCTTCCCTTTCCCTGCTTCATT

	44960	44970	44980	44990	45000
AF121782	CTCTTCTCCTCCATCTTGCTTCTTCTGGTTAAGACTGATAG				
	GAGAAAGAGGAAGGTAGAAACGAAAGGAAAAAGACCAATTCTGACTATC				
	720	730	740	750	
1. SEQ05_ORF710	AGGTTTTCATTCGCCTACTTG--GGGCAAAGTTGGACTT-GGACTAGCAG>				
[1596]					
AF121782	CTCTTCTCCTCCATCTTGCTTCTTCTGGTTAAGACTGATAG				
	45010	45020	45030	45040	45050
AF121782	AGACAGATTTATCACTTCCCCTTGAAATCCATTAGTATTAAACAGCC				
	TCTGTCTAAAATAGTGAAGGGAAACTTAGTAAAATCATAAATTGTCGG				
	760	770	780	790	800
1. SEQ05_ORF	GCACCATGCTCTGAC-GCCGACGTGTA-CTCTTACAATACGCTGCTG-C>				
[1596]					
AF121782	AGACAGATTTATCACTTCCCCTTGAAATCCATTAGTATTAAACAGCC				
	45060	45070	45080	45090	45100
AF121782	TTTCTGGAAACGTATCCTGGAATTCTCTAGGGCCAGTTGCAGTCATTAA				
	AAAGACCTTGCATAGGACCTAAGAAGATCCGGTCAACGTCAGTAAA				
	C				
1. SEQ05_ORF	810	820	830	840	
[1596]	T-GCTGCCGCCGTGTTG-TGGCTGCAACTG-CTGCTGCCGTTGTTGT>				
AF121782	TTTCTGGAAACGTATCCTGGAATTCTCTAGGGCCAGTTGCAGTCATTAA				
	45110	45120	45130	45140	45150
AF121782	TCTTGATTTAGAGACAGTTGTCAATCACTGCCCTTCTCTAGTTTCC				
	AGAAAACAAATCTGTCAACAGTTAGTGACGGAAAGAGATCAAAAGG				
	AAG				
1. SEQ05_O850	860	870	880	890	900
[1596]	T-TCTGCTGTAGAAAAAGAGGATTCGTATTCAATTCAAAAGATCTGAA>				
AF121782	TCTTGATTTAGAGACAGTTGTCAATCACTGCCCTTCTCTAGTTTCC				
	45160	45170	45180	45190	45200
AF121782	ATATACATGACTATATTCTCTGCTTGCATCATTATCAACTCTGAAGCA				
	TATATGTACTGATATAAGAGACGAACGTTAGTAAATAGTTGAGACTTCGT				
	910	920	930	940	950
1. SEQ05_ORF	AAAGAGAAGAC-AAACAAAGAAC-TGAGACAGAAAGTGGAAATGAAAAC>				
[1596]					
AF121782	ATATACATGACTATATTCTCTGCTTGCATCATTATCAACTCTGAAGCA				

	45210	45220	45230	45240	45250
AF121782	TGCTTTAACTCTTCCTCTTCCAGCAGAATCCCCCAACTTATTCCTCT ACGAAATTGAGAAAGGAGAAAGGTCGTCTAGGGGGTTGAATAAAGAGA				
			CC		
1. SEQ05_ORF	960	970		990	1000
[1596]	TCCGGCTAC-AATTCAAGATGAACAAAAGAACAGAAACCGCTCTCCCT> 				
AF121782	TGCTTTAACTCTTCCTCTTCCAGCAGAATCCCCCAACTTATTCCTCT				
	45260	45270	45280	45290	45300
AF121782	ACCCGCCTCCAACACTACAGTGGGATAGTCATTATAGTCAAAGTTGTGTGT TGGGACGGAGGTTGATGTCACCCTATCAGTAATATCAGTTCAACACACA				
	A			AGC	GGCC
1. SEQ05_ORF	1010	1020	1030	1040	1050
[1596]	CCCAATCCTGTGAATCCAGT--GATCCTGAACAAAGAACAGTTGTCTCC> 				
AF121782	ACCCGCCTCCAACACTACAGTGGGATAGTCATTATAGTCAAAGTTGTGTGT				
	45310	45320	45330	45340	45350
AF121782	TCACCAAATATATCAAGTCATTGAGAGAAAAGAAAAGAACATAAACAAAATT AGTGGTTATATAGTCAGTAACCTCTTTCTTTCTTATTGTTAA				
	GCG	C			
1. SEQ05_O1060	1070	1080	1090	1100	1110
[1596]	TCACCAAGGCTGATCAAGTC-CACCCAGGCCAGCAAGTCATCCAC-AGGCT> 				
AF121782	TCACCAAATATATCAAGTCATTGAGAGAAAAGAAAAGAACATAAACAAAATT				
	45360	45370	45380	45390	45400
AF121782	TATAATAATAGCTTATTTTCATTTAGAGGTAATTGGAGGTGCTGAAG ATATTATTATCGAATAAAAGTAAAATCTCCATAAACCTCCACGACTTC				
	1120	1130	1140	1150	
1. SEQ05_ORF					
[1596]	TCTTTAAT--CTGGCCAGTCCTGAGA-AGGTCAGTAATA-CAACTGTAG> 				
AF121782	TATAATAATAGCTTATTTTCATTTAGAGGTAATTGGAGGTGCTGAAG				
	45410	45420	45430	45440	45450
AF121782	ATAATGTTACACAGTAAAAAGTAAAAGGATGCTTACAAAGATTGGAA TATTACAATGTGTCACTTTCTACGAAATGTTCTAAACCTT				
	1. SEQ05_ORF				
[1596]	-TA> 				
AF121782	ATA				

45460 45470 45480 45490 45500
AF121782 TAGTCTTACCAAAATTAATCACTTGCATTCTTAAAAGTGTATTTATA
ATCAGAATGGTTTAAATTAGTGAAACGTAAGAAATTTCACATAAATAT